



SEQUENCE LISTING

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GOODNOW, CHRISTOPHER CARL

<120> CARD11 NF κ B ACTIVATING POLYPEPTIDES, NUCLEIC ACIDS, INBRED
AND TRANSGENIC ANIMALS, AND METHODS OF USE THEREOF

<130> 022731/0502

<140> 10/632,696
<141> 2003-08-01

<150> US 60/401,078
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<151> 2002-10-29

<160> 35

<170> PatentIn Ver. 2.1

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Ile Asp Glu Gln Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu Pro
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Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr Lys Gly Gln Arg Gly
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Lys Leu Val Thr Gly Lys Glu Pro Thr Arg Arg Phe Ser Thr Ile Val
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aag cag ctg agc ctg ata cgg gtg gag ctg ctg acc ttc cag gag cga	530	
Lys Gln Leu Ser Leu Ile Arg Val Glu Leu Leu Thr Phe Gln Glu Arg		
160	165	170

tac tac aag atg aag gag gag cgg gac agc tac aat gac gag ctc gtc	578	
Tyr Tyr Lys Met Lys Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val		
175	180	185

aag gtc aag gac gac aac tac aac tta gcc atg cgc tac gcc cag ctc	626	
Lys Val Lys Asp Asp Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu		
190	195	200

agt gag gag aaa aac atg gcg gtg atg agg agc cgc gac ctc caa ctc		674
Ser Glu Glu Lys Asn Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu		
205 210 215 220		
gag atc gac cag ctc aaa cac cga ctg aac aag atg gag gag gaa tgc		722
Glu Ile Asp Gln Leu Lys His Arg Leu Asn Lys Met Glu Glu Cys		
225 230 235		
aag ctg gag aga aat cag tcc ctc aag ctc aag aat gac atc gag aac		770
Lys Leu Glu Arg Asn Gln Ser Leu Lys Leu Lys Asn Asp Ile Glu Asn		
240 245 250		
cgg ccc agg aag gag cag gtc ctg gag ctg gag cgg gag aat gag atg		818
Arg Pro Arg Lys Glu Gln Val Leu Glu Leu Glu Arg Glu Asn Glu Met		
255 260 265		
ctg aag acg aaa att cag gag ctg cag tcc atc atc cag gct ggc aag		866
Leu Lys Thr Lys Ile Gln Glu Leu Gln Ser Ile Ile Gln Ala Gly Lys		
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cgc agc ctc cct gac tca gac aag gcc atc ttg gac atc cag gaa cat		914
Arg Ser Leu Pro Asp Ser Asp Lys Ala Ile Leu Asp Ile Gln Glu His		
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gac cgg aag gag gcg cta gag gac cgg cag gaa ctg gtc aac aaa att		962
Asp Arg Lys Glu Ala Leu Glu Asp Arg Gln Glu Leu Val Asn Lys Ile		
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Tyr Asn Leu Gln Glu Glu Val Arg Gln Ala Glu Glu Leu Arg Asp Lys		
320 325 330		
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Tyr Leu Glu Glu Lys Glu Asp Leu Glu Leu Lys Cys Ser Thr Leu Gly		
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Lys Asp Cys Glu Met Tyr Lys His Arg Met Asn Thr Val Met Leu Gln		
350 355 360		
ctg gag gag gtg gag cgg gag cgg gac cag gcc ttc cac tcc cga gat		1154
Leu Glu Glu Val Glu Arg Glu Arg Asp Gln Ala Phe His Ser Arg Asp		
365 370 375 380		
gag gca cag aca cag tac tca cag tgc tta atc gag aag gac aag tac		1202
Glu Ala Gln Thr Gln Tyr Ser Gln Cys Leu Ile Glu Lys Asp Lys Tyr		
385 390 395		
cg ^g aag cag atc cg ^g gag ctg gag gag aag aac gat gag atg cgt att		1250
Arg Lys Gln Ile Arg Glu Leu Glu Glu Lys Asn Asp Glu Met Arg Ile		
400 405 410		
gag atg gtg agg agg gag gcc tgt att gtc aac ctg gaa agc aag ctc		1298
Glu Met Val Arg Arg Glu Ala Cys Ile Val Asn Leu Glu Ser Lys Leu		
415 420 425		

cgg cgc ctg tcc aag gac aac ggc agc ctc gac cag agt ctg cct aga Arg Arg Leu Ser Lys Asp Asn Gly Ser Leu Asp Gln Ser Leu Pro Arg 430 435 440	1346
cac ctt cca gcc acc atc atc tca cag aac ctt gga gac acc agc ccc His Leu Pro Ala Thr Ile Ile Ser Gln Asn Leu Gly Asp Thr Ser Pro 445 450 455 460	1394
agg acc aat ggc cag gaa gct gat gat tct tca acc tca gaa gag tct Arg Thr Asn Gly Gln Glu Ala Asp Asp Ser Ser Thr Ser Glu Glu Ser 465 470 475	1442
ccc gaa gac agc aag tac ttt ctg cct tac cac cca ccc cgg cgc cgg Pro Glu Asp Ser Lys Tyr Phe Leu Pro Tyr His Pro Pro Arg Arg Arg 480 485 490	1490
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gat gcg cca cac cgg agc acg gtg gaa gaa gac aac gat agc tgt ggg Asp Ala Pro His Arg Ser Thr Val Glu Glu Asp Asn Asp Ser Cys Gly 575 580 585	1778
ttt gat gcc tta gac ctt gac gat gaa aat cac gaa cgt tat tcc ttt Phe Asp Ala Leu Asp Leu Asp Asp Glu Asn His Glu Arg Tyr Ser Phe 590 595 600	1826
gga cct ccc tcc atc cac tcc tcc tct tca cac cag tca gag gga Gly Pro Pro Ser Ile His Ser Ser Ser Ser His Gln Ser Glu Gly 605 610 615 620	1874
ctg gat gcc tac gac ctg gag cag gtc aac ctc atg tta cga aag ttc Leu Asp Ala Tyr Asp Leu Glu Gln Val Asn Leu Met Leu Arg Lys Phe 625 630 635	1922
tct ttg gaa agg ccc ttc cgg cca tcg gtc aca tct ggg ggt cac gtg Ser Leu Glu Arg Pro Phe Arg Pro Ser Val Thr Ser Gly Gly His Val 640 645 650	1970

cg g ggc acc ggg ccc ttg gtc cag cac aca act ctg aat ggc gat ggg Arg Gly Thr Gly Pro Leu Val Gln His Thr Thr Leu Asn Gly Asp Gly 655 660 665	2018
c t atc acg cag ctc acc ctt ctg ggc ggc aat gca cgc ggg agc ttc Leu Ile Thr Gln Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly Ser Phe 670 675 680	2066
att cac tct gtc aag cca ggc tca ctg gct gag agg gcc gga ctg cgt Ile His Ser Val Lys Pro Gly Ser Leu Ala Glu Arg Ala Gly Leu Arg 685 690 695 700	2114
gag ggc cac caa ctc ctg ctg gaa ggt tgc atc cga ggc gaa agg Glu Gly His Gln Leu Leu Leu Glu Gly Cys Ile Arg Gly Glu Arg 705 710 715	2162
cag agc gtt cca ctg gat gcg tgc aca aaa gaa gag gcc cgt tgg acc Gln Ser Val Pro Leu Asp Ala Cys Thr Lys Glu Glu Ala Arg Trp Thr 720 725 730	2210
atc cag agg tgc agt ggc ctc atc act ctg cat tac aag gtc aac cat Ile Gln Arg Cys Ser Gly Leu Ile Thr Leu His Tyr Lys Val Asn His 735 740 745	2258
gaa gga tac cgg aag ctg ctg aag gag atg gag gat ggt ctg atc aca Glu Gly Tyr Arg Lys Leu Leu Lys Glu Met Glu Asp Gly Leu Ile Thr 750 755 760	2306
tca ggg gac tcg ttc tat atc cgc ctg aac ctg aac atc tcc agc cag Ser Gly Asp Ser Phe Tyr Ile Arg Leu Asn Leu Asn Ile Ser Ser Gln 765 770 775 780	2354
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cta gac acc atg tac cag gac agg cac gag tgg ctg tgt gca cga gtc Leu Asp Thr Met Tyr Gln Asp Arg His Glu Trp Leu Cys Ala Arg Val 800 805 810	2450
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ctc cgg aac acc ctg cag ccc gaa gag atg ctt tcg acg agc gac ccc Leu Arg Asn Thr Leu Gln Pro Glu Glu Met Leu Ser Thr Ser Asp Pro 865 870 875	2642

cga gtc agc ccc cgc ctc tcc aga gcg agt ttc ttc ttt ggc cag ctc Arg Val Ser Pro Arg Leu Ser Arg Ala Ser Phe Phe Phe Gly Gln Leu 880 885 890	2690
ctg cag ttt gtc agc cg ^g tca gaa aac aag tac aaa aga atg aac agc Leu Gln Phe Val Ser Arg Ser Glu Asn Lys Tyr Lys Arg Met Asn Ser 895 900 905	2738
aat gag cgc gtg aga atc atc tct ggg agt ccc ctg ggg agc ctc tcc Asn Glu Arg Val Arg Ile Ile Ser Gly Ser Pro Leu Gly Ser Leu Ser 910 915 920	2786
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acg ccc acc atg ctg gcc aag aca ttg gtg cag aag ctg ctc aac tca Thr Pro Thr Met Leu Ala Lys Thr Leu Val Gln Lys Leu Leu Asn Ser 975 980 985	2978
ggg ggt gcc atg gag ttc acc atc tgc aag tca gat att gtc aca aga Gly Gly Ala Met Glu Phe Thr Ile Cys Lys Ser Asp Ile Val Thr Arg 990 995 1000	3026
gat gag ttc ctc cga aag cag aag aca gag acc atc atc tac tcc cg ^g Asp Glu Phe Leu Arg Lys Gln Lys Thr Glu Thr Ile Ile Tyr Ser Arg 1005 1010 1015 1020	3074
gaa aag aac ccc aac acc ttt gaa tgc atc gtc cct gcc aac att gag Glu Lys Asn Pro Asn Thr Phe Glu Cys Ile Val Pro Ala Asn Ile Glu 1025 1030 1035	3122
gct gtg gca gcc aag aac aaa cac tgc ctg ctg gag gct ggg atc ggc Ala Val Ala Ala Lys Asn Lys His Cys Leu Leu Glu Ala Gly Ile Gly 1040 1045 1050	3170
tgt gtg cgc gac ctg atc aag tgc aag gtg tac ccc ata gtg ctg ctc Cys Val Arg Asp Leu Ile Lys Cys Lys Val Tyr Pro Ile Val Leu Leu 1055 1060 1065	3218
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cg ^g cca gag acg gaa gag gaa ttc ctg cga gtg tgc agg ctc aaa gag Arg Pro Glu Thr Glu Glu Phe Leu Arg Val Cys Arg Leu Lys Glu 1085 1090 1095 1100	3314

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gta gag gag cag cgc aag acc atc tgg gtg gac gag gac cag ctg Val Glu Glu Gln Arg Lys Thr Ile Trp Val Asp Glu Asp Gln Leu 1135	1140	1145	3455
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Asp Asn Val Glu Cys Asn Arg His Met Leu Ser Arg Tyr Ile Asn Pro 20	25	30	
Ala Lys Leu Thr Pro Tyr Leu Arg Gln Cys Lys Val Ile Asp Glu Gln 35	40	45	
Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu Pro Ser Lys Ile Asn 50	55	60	
Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr Lys Gly Gln Arg Gly 65	70	75	80
Tyr Val Val Phe Leu Glu Ser Leu Glu Phe Tyr Tyr Pro Glu Leu Tyr 85	90	95	
Lys Leu Val Thr Gly Lys Glu Pro Thr Arg Arg Phe Ser Thr Ile Val 100	105	110	
Val Glu Glu Gly His Glu Gly Leu Thr His Phe Leu Met Asn Glu Val 115	120	125	
Ile Lys Leu Gln Gln Val Lys Ala Lys Asp Leu Gln Arg Cys Glu 130	135	140	
Leu Leu Ala Lys Ser Arg Gln Leu Glu Asp Glu Lys Lys Gln Leu Ser 145	150	155	160
Leu Ile Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met 165	170	175	
Lys Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp 180	185	190	

Asp Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys
 195 200 205

Asn Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu Glu Ile Asp Gln
 210 215 220

Leu Lys His Arg Leu Asn Lys Met Glu Glu Glu Cys Lys Leu Glu Arg
 225 230 235 240

Asn Gln Ser Leu Lys Leu Lys Asn Asp Ile Glu Asn Arg Pro Arg Lys
 245 250 255

Glu Gln Val Leu Glu Leu Glu Arg Glu Asn Glu Met Leu Lys Thr Lys
 260 265 270

Ile Gln Glu Leu Gln Ser Ile Ile Gln Ala Gly Lys Arg Ser Leu Pro
 275 280 285

Asp Ser Asp Lys Ala Ile Leu Asp Ile Gln Glu His Asp Arg Lys Glu
 290 295 300

Ala Leu Glu Asp Arg Gln Glu Leu Val Asn Lys Ile Tyr Asn Leu Gln
 305 310 315 320

Glu Glu Val Arg Gln Ala Glu Glu Leu Arg Asp Lys Tyr Leu Glu Glu
 325 330 335

Lys Glu Asp Leu Glu Leu Lys Cys Ser Thr Leu Gly Lys Asp Cys Glu
 340 345 350

Met Tyr Lys His Arg Met Asn Thr Val Met Leu Gln Leu Glu Glu Val
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Glu Arg Glu Arg Asp Gln Ala Phe His Ser Arg Asp Glu Ala Gln Thr
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Gln Tyr Ser Gln Cys Leu Ile Glu Lys Asp Lys Tyr Arg Lys Gln Ile
 385 390 395 400

Arg Glu Leu Glu Glu Lys Asn Asp Glu Met Arg Ile Glu Met Val Arg
 405 410 415

Arg Glu Ala Cys Ile Val Asn Leu Glu Ser Lys Leu Arg Arg Leu Ser
 420 425 430

Lys Asp Asn Gly Ser Leu Asp Gln Ser Leu Pro Arg His Leu Pro Ala
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Thr Ile Ile Ser Gln Asn Leu Gly Asp Thr Ser Pro Arg Thr Asn Gly
 450 455 460

Gln Glu Ala Asp Asp Ser Ser Thr Ser Glu Glu Ser Pro Glu Asp Ser
 465 470 475 480

Lys Tyr Phe Leu Pro Tyr His Pro Pro Arg Arg Arg Met Asn Leu Lys
 485 490 495

Gly Ile Gln Leu Gln Arg Ala Lys Ser Pro Ile Ser Met Lys Gln Ala
 500 505 510

Ser Glu Phe Gln Val Lys Gly His Glu Glu Asp Phe Thr Asp Gly Ser
 515 520 525

Pro Ser Ser Ser Arg Ser Leu Pro Val Thr Ser Ser Phe Ser Lys Met
 530 535 540

Gln Pro His Arg Ser Arg Ser Ser Ile Met Ser Ile Thr Ala Glu Pro
 545 550 555 560

Pro Gly Asn Asp Ser Ile Val Arg Arg Cys Lys Glu Asp Ala Pro His
 565 570 575

Arg Ser Thr Val Glu Glu Asp Asn Asp Ser Cys Gly Phe Asp Ala Leu
 580 585 590

Asp Leu Asp Asp Glu Asn His Glu Arg Tyr Ser Phe Gly Pro Pro Ser
 595 600 605

Ile His Ser Ser Ser Ser His Gln Ser Glu Gly Leu Asp Ala Tyr
 610 615 620

Asp Leu Glu Gln Val Asn Leu Met Leu Arg Lys Phe Ser Leu Glu Arg
 625 630 635 640

Pro Phe Arg Pro Ser Val Thr Ser Gly Gly His Val Arg Gly Thr Gly
 645 650 655

Pro Leu Val Gln His Thr Thr Leu Asn Gly Asp Gly Leu Ile Thr Gln
 660 665 670

Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly Ser Phe Ile His Ser Val
 675 680 685

Lys Pro Gly Ser Leu Ala Glu Arg Ala Gly Leu Arg Glu Gly His Gln
 690 695 700

Leu Leu Leu Glu Gly Cys Ile Arg Gly Glu Arg Gln Ser Val Pro
 705 710 715 720

Leu Asp Ala Cys Thr Lys Glu Glu Ala Arg Trp Thr Ile Gln Arg Cys
 725 730 735

Ser Gly Leu Ile Thr Leu His Tyr Lys Val Asn His Glu Gly Tyr Arg
 740 745 750

Lys Leu Leu Lys Glu Met Glu Asp Gly Leu Ile Thr Ser Gly Asp Ser
 755 760 765

Phe Tyr Ile Arg Leu Asn Leu Asn Ile Ser Ser Gln Leu Asp Ala Cys
 770 775 780

Ser Met Ser Leu Lys Cys Asp Asp Val Val His Val Leu Asp Thr Met
 785 790 795 800

Tyr Gln Asp Arg His Glu Trp Leu Cys Ala Arg Val Asp Pro Phe Thr
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 Asp Gln Asp Leu Asp Thr Gly Thr Ile Pro Ser Tyr Ser Arg Ala Gln
 820 825 830
 Gln Leu Leu Leu Val Lys Leu Gln Arg Leu Val His Arg Gly Asn Arg
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 Glu Glu Ala Asp Ser Ala His His Thr Leu Arg Ser Leu Arg Asn Thr
 850 855 860
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 865 870 875 880
 Arg Leu Ser Arg Ala Ser Phe Phe Phe Gly Gln Leu Leu Gln Phe Val
 885 890 895
 Ser Arg Ser Glu Asn Lys Tyr Lys Arg Met Asn Ser Asn Glu Arg Val
 900 905 910
 Arg Ile Ile Ser Gly Ser Pro Leu Gly Ser Leu Ser Arg Ser Ser Leu
 915 920 925
 Asp Ala Thr Lys Leu Leu Thr Glu Lys His Glu Glu Leu Asp Pro Glu
 930 935 940
 Asn Glu Leu Ser Arg Asn Leu Thr Leu Ile Pro Tyr Ser Leu Val Arg
 945 950 955 960
 Ala Phe His Cys Glu Arg Arg Pro Val Leu Phe Thr Pro Thr Met
 965 970 975
 Leu Ala Lys Thr Leu Val Gln Lys Leu Leu Asn Ser Gly Gly Ala Met
 980 985 990
 Glu Phe Thr Ile Cys Lys Ser Asp Ile Val Thr Arg Asp Glu Phe Leu
 995 1000 1005
 Arg Lys Gln Lys Thr Glu Thr Ile Ile Tyr Ser Arg Glu Lys Asn Pro
 1010 1015 1020
 Asn Thr Phe Glu Cys Ile Val Pro Ala Asn Ile Glu Ala Val Ala Ala
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 Lys Asn Lys His Cys Leu Leu Glu Ala Gly Ile Gly Cys Val Arg Asp
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 1060 1065 1070
 Glu Lys Asn Ile Lys Arg Phe Arg Lys Leu Leu Pro Arg Pro Glu Thr
 1075 1080 1085
 Glu Glu Glu Phe Leu Arg Val Cys Arg Leu Lys Glu Lys Glu Leu Glu
 1090 1095 1100

Ala Leu Pro Cys Leu Tyr Ala Thr Val Glu Ala Glu Met Trp Ser Ser
 1105 1110 1115 1120
 Val Glu Glu Leu Leu Arg Val Leu Lys Asp Lys Ile Val Glu Glu Gln
 1125 1130 1135
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15

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Gln Gly Glu Leu Gln Trp Ala Glu Glu Leu Arg Asp Lys Tyr Leu Gln
35 40 45

Glu Met Glu Asp Leu Arg Leu Lys His Arg Thr Leu Leu Lys Asp Cys
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Asp Leu Tyr Lys His Arg
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Gln Glu Ala Arg Gln Ala Glu Glu Leu Arg Asp Lys Tyr Leu Glu
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Glu Met Tyr Lys His Arg
 65 70

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Arg Glu Arg Ala Val Ala Ala Glu Arg Gln Arg Glu Gln Tyr Trp Glu
 35 40 45

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Arg Lys Asp Leu Arg Gln Gly Glu Ala Arg Arg Leu Arg Cys Met Glu
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Glu Met Tyr Lys His Arg
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ttactaccca gaactttaca aactggtgac tgaaaaggaa cccacccgga gattctccac 180
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agccaaggac cttcagcgct gtgagctgtt ggccttcc caactgg aggatgagaa 180
gaagcagctt agcctgatac ggggtggagct gtgaccttc caggagcgat actacaagat 240
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cttagccatg cgtacgccc agtcagtga ggagaaaaac atggcggtga tgaggagccg 360
cgacctccaa ctcgaggtgg ggtatgcctgg gctccggctg aactgaggaa agggaaaaga 420
aatgtct 427

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<213> Mus sp.

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cgcttagagga cccggcaggaa ctggtaaca aaatttacaa cctacaagag gaagtccggc 180
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 19
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aggcctgtat tgtcaacctg gaaagcaagc tccggcgct gtccaaggac aacggcagcc 240
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<210> 20
<211> 185
<212> DNA
<213> Homo sapiens

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<211> 145
<212> DNA
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<210> 22
<211> 183
<212> DNA
<213> Homo sapiens

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<211> 153
<212> DNA
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<210> 25
<211> 233
<212> DNA
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gggactggat gcctacgacc tggagcaggt caacctcatg ttacgaaagt tctcttgg 180
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ct 302

<210> 27
<211> 228

<212> DNA

<213> Homo sapiens

<400> 27

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ggaccatcca gaggtgcagt ggcctcatca ctgcattt caaggtcaac catgaaggta 180
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<210> 28

<211> 342

<212> DNA

<213> Homo sapiens

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ggtgcatgtc cttagacacca tgttaccagga caggcacgag tggctgtgtg caccgatcga 240
ccccttcaact gaccaagacc tggacacggg caccatcccc agctacagcc ggtgagtggg 300
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<210> 29

<211> 197

<212> DNA

<213> Homo sapiens

<400> 29

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gctcaccaca ccctgcgcag cctccgggtt ggtacacaaa gacacacaca cacacagccc 180
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<210> 30

<211> 196

<212> DNA

<213> Homo sapiens

<400> 30

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gtttctctt tggccagctc ctgcaggtaa ggttgggtat cgatgccc ctgactttc 180
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<210> 31

<211> 236

<212> DNA

<213> Homo sapiens

<400> 31

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gtccctggg gaggctctcc cggcctcgc tggatgccac caaactcctg accgagaagc 180

atgaagggtgt gtgacgacct cgaggccccca ccccacagcc cagcaggggc atgtct 236

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<211> 280
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<213> Homo sapiens

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ctgtgagcgc cgccaggcctg tgctcttcac gccaccatg ctggccaaga cattggtgca 180
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<210> 33
<211> 225
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<210> 34
<211> 216
<212> DNA
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tagtgcgtct catccgggtg agcgagaaga acatcaaacg gttcaggtaa ggacacccag 180
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<210> 35
<211> 291
<212> DNA
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gaggcgctgc cctgcctcta cgccaccgtg gaagctgaga tgtggagcag cgtggaggag 180
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